



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/051,644C

DATE: 10/01/2004

TIME: 11:08:15

Input Set : A:\Cam-0121.app

Output Set: N:\CRF4\10012004\J051644C.raw

3 <110> APPLICANT: Liu, et al.  
 5 <120> TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling  
 6 Parasitic Nematodes  
 8 <130> FILE REFERENCE: 2002630-0012  
 10 <140> CURRENT APPLICATION NUMBER: 10/051,644C  
 11 <141> CURRENT FILING DATE: 2002-01-18  
 13 <160> NUMBER OF SEQ ID NOS: 8  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 425  
 19 <212> TYPE: PRT  
 20 <213> ORGANISM: Artificial Sequence  
 22 <220> FEATURE:  
 23 <223> OTHER INFORMATION: Description of Artificial Sequence:VAP-1 Amino  
 24 Acid Sequence  
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 31 20 25 30  
 33 Arg Lys Met Phe Tyr Asp Ala His Asn Asp Ala Arg Arg Ser Met Ala  
 34 35 40 45  
 36 Lys Gly Leu Glu Pro Asn Lys Cys Gly Leu Leu Ser Gly Gly Lys Asn  
 37 50 55 60  
 39 Val Tyr Glu Leu Asn Trp Asp Cys Glu Met Glu Ala Lys Ala Gln Glu  
 40 65 70 75 80  
 42 Trp Ala Asp Gly Cys Pro Ser Ser Phe Gln Thr Phe Asp Pro Thr Trp  
 43 85 90 95  
 45 Gly Gln Asn Tyr Ala Thr Tyr Met Gly Ser Ile Ala Asp Pro Leu Pro  
 46 100 105 110  
 48 Tyr Ala Ser Met Ala Val Asn Gly Trp Trp Ser Glu Ile Arg Thr Val  
 49 115 120 125  
 51 Gly Leu Thr Asp Pro Asp Asn Lys Tyr Thr Asn Ser Ala Met Phe Arg  
 52 130 135 140  
 54 Phe Ala Asn Met Ala Asn Gly Lys Ala Ser Ala Phe Gly Cys Ala Tyr  
 55 145 150 155 160  
 57 Ala Leu Cys Ala Gly Lys Leu Ser Ile Asn Cys Ile Tyr Asn Lys Ile  
 58 165 170 175  
 60 Gly Tyr Met Thr Asn Ala Ile Ile Tyr Glu Lys Gly Asp Ala Cys Thr  
 61 180 185 190  
 63 Ser Asp Ala Glu Cys Thr Thr Tyr Ser Asp Ser Gln Cys Lys Asn Gly  
 64 195 200 205  
 66 Leu Cys Tyr Lys Ala Pro Gln Ala Pro Val Val Glu Thr Phe Thr Met

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67 210 215 220  
 69 Cys Pro Ser Val Thr Asp Gln Ser Asp Gln Ala Arg Gln Asn Phe Leu  
 70 225 230 235 240  
 72 Asp Thr His Asn Lys Leu Arg Thr Ser Leu Ala Lys Gly Leu Glu Ala  
 73 245 250 255  
 75 Asp Gly Ile Ala Ala Gly Ala Phe Ala Pro Met Ala Lys Gln Met Pro  
 76 260 265 270  
 78 Lys Leu Val Lys Tyr Ser Cys Thr Val Glu Ala Asn Ala Arg Thr Trp  
 79 275 280 285  
 81 Ala Lys Gly Cys Leu Tyr Gln His Ser Thr Ser Ala Gln Arg Pro Gly  
 82 290 295 300  
 84 Leu Gly Glu Asn Leu Tyr Met Ile Ser Ile Asn Asn Met Pro Lys Ile  
 85 305 310 315 320  
 87 Gln Thr Ala Glu Asp Ser Ser Lys Ala Trp Trp Ser Glu Leu Lys Asp  
 88 325 330 335  
 90 Phe Gly Val Gly Ser Asp Asn Ile Leu Thr Gln Ala Val Phe Asp Arg  
 91 340 345 350  
 93 Gly Val Gly His Tyr Thr Gln Met Ala Trp Glu Gly Thr Thr Glu Ile  
 94 355 360 365  
 96 Gly Cys Phe Val Glu Asn Cys Pro Thr Phe Thr Tyr Ser Val Cys Gln  
 97 370 375 380  
 99 Tyr Gly Pro Ala Gly Asn Tyr Met Asn Gln Leu Ile Tyr Thr Lys Gly  
 100 385 390 395 400  
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 116 Nucleotide Sequence  
 118 <400> SEQUENCE: 2  
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 120 ttcggctgt ctaacaccaa gatcaatgac caggctcgta agatgttcta ttagtgcac 120  
 121 aatgatgcaa gacgaagcat ggctaaaggg cttgagccaa acaagtgcgg actcttatct 180  
 122 ggtggaaaga atgttatga attgaattgg gattgcgaga tggaaagcaaa agtcaggaa 240  
 123 tgggcagacg gatgtccca gctttccag acatttgc acacatgggg gcagaactac 300  
 124 ggcacgtaca tggatcgat tgctgatccg cttccatacg cttccatggc tggtaatggg 360  
 125 tggtggtcg aaattagaac cgtaggactt acggatcctg ataacaagta cactaacagt 420  
 126 gcaatgttcc gatttgctaa tatggcaat ggtaaagctt cagctttgg atgtgcatac 480  
 127 gcgttgcg caggaaaact atccatcaat tgcattaca acaagatagg atacatgacc 540  
 128 aatgctatca tttatgaaaa aggagatgcc tgtaccagt acgctgaatg caccacctac 600  
 129 tcagactcac aatgcaaaaa cggtcttgc tataaggcac ctcaagctcc agtcgttgag 660  
 130 actttcacaa tgtgcccttc ggtcacggac cagtcggatc aggccgcgtca aaacttcttg 720  
 131 gacaccata acaaattgcg tacaaggc ttgaagctga tggaaattgcc 780  
 132 gctggagcat ttgcaccaat ggccaagcaa atgccaaaac tggtaaataa cagctgcaca 840

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133 gttgaagcaa acgccagaac atgggcaaaa ggatgcctt accagcattc aacaagcgca 900  
 134 cagagaccag gactcggta aatctttat atgatcagca ttaacaacat gcctaaaatt 960  
 135 caaaccgcgg aggactcctc aaaggcttgg tggccgagt tgaaagactt cggagtcgg 1020  
 136 tctgacaaca ttctgaccca agcagtttt gatcgtggcg ttggacatta cacacaaatg 1080  
 137 gcatggaaag gaactactga aattggatgt tttgtggaga attgtccaac attcaattat 1140  
 138 tccgtatgcc aatatggcc agcgggaaac tacatgaacc aactaatcta taccaaggc 1200  
 139 tcaccatgca cagctgacgc cgattgcca ggaaccaga catgcagtgt cgctgaagca 1260  
 140 ttatgtgtta tcccttagta aattttctat gcaactctt gaaagtctata ataaatatgc 1320  
 141 aaaaattaaa aaaaaaaaaa a 1341  
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 146 <212> TYPE: PRT  
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 151 Acid Sequence  
 153 <400> SEQUENCE: 3  
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 158 20 25 30  
 160 Glu Gln Asn Val Trp Asn Asp Val Asp Asp Lys Val Val Glu Ala Leu  
 161 35 40 45  
 163 Gly Gly Leu Asp Asp Glu Leu Leu Thr Glu His Val Cys Asn Lys Ser  
 164 50 55 60  
 166 Thr Ile Thr Gln Leu Gln Glu Ile Ile Leu Thr Thr His Asn Glu  
 167 65 70 75 80  
 169 Leu Arg Arg Ser Leu Ala Phe Gly Lys Gln Arg Asn Lys Arg Gly Leu  
 170 85 90 95  
 172 Met Asn Gly Ala Arg Asn Met Tyr Lys Leu Asp Trp Asp Cys Glu Leu  
 173 100 105 110  
 175 Ala Ser Leu Ala Ala Asn Trp Ser Thr Ser Cys Pro Gln His Phe Met  
 176 115 120 125  
 178 Pro Gln Ser Val Leu Gly Ser Asn Ala Gln Leu Phe Lys Arg Phe Tyr  
 179 130 135 140  
 181 Phe Tyr Phe Asp Gly His Asp Ser Thr Val His Met Arg Asn Ala Met  
 182 145 150 155 160  
 184 Lys Tyr Trp Trp Gln Gln Gly Glu Glu Lys Gly Asn Glu Asp Gln Lys  
 185 165 170 175  
 187 Asn Arg Phe Tyr Ala Arg Arg Asn Tyr Phe Gly Trp Ala Asn Met Ala  
 188 180 185 190  
 190 Lys Gly Lys Thr Tyr Arg Val Gly Cys Ser Tyr Ile Met Cys Gly Asp  
 191 195 200 205  
 193 Gly Glu Ser Ala Leu Phe Thr Cys Leu Tyr Asn Glu Lys Ala Gln Cys  
 194 210 215 220  
 196 Glu Lys Glu Met Ile Tyr Glu Asn Gly Lys Pro Cys Cys Glu Asp Lys  
 197 225 230 235 240  
 199 Asp Cys Phe Thr Tyr Pro Gly Ser Lys Cys Leu Val Pro Glu Gly Leu  
 200 245 250 255

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202 Cys Gln Ala Pro Ser Met Val Lys Asp Asp Gly Gly Ser Phe Gln Cys  
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205 Asp Asn Ser Leu Val Ser Asp Val Thr Arg Asn Phe Thr Leu Glu Gln  
206 275 280 285  
208 His Asn Phe Tyr Arg Ser Arg Leu Ala Lys Gly Phe Glu Trp Asn Gly  
209 290 295 300  
211 Glu Thr Asn Thr Ser Gln Pro Lys Ala Ser Gln Met Ile Lys Met Glu  
212 305 310 315 320  
214 Tyr Asp Cys Met Leu Glu Arg Phe Ala Gln Asn Trp Ala Asn Asn Cys  
215 325 330 335  
217 Val Phe Ala His Ser Ala His Tyr Glu Arg Pro Asn Gln Gly Gln Asn  
218 340 345 350  
220 Leu Tyr Met Ser Ser Phe Ser Asn Pro Asp Pro Arg Ser Leu Ile His  
221 355 360 365  
223 Thr Ala Val Glu Lys Trp Trp Gln Glu Leu Glu Glu Phe Gly Thr Pro  
224 370 375 380  
226 Ile Asp Asn Val Leu Thr Pro Glu Leu Trp Asp Leu Lys Gly Lys Ala  
227 385 390 395 400  
229 Ile Gly His Tyr Thr Gln Met Ala Trp Asp Arg Thr Tyr Arg Leu Gly  
230 405 410 415  
232 Cys Gly Ile Ala Asn Cys Pro Lys Met Ser Tyr Val Val Cys His Tyr  
233 420 425 430  
235 Gly Pro Ala Gly Asn Arg Lys Asn Asn Lys Ile Tyr Glu Ile Gly Asp  
236 435 440 445  
238 Pro Cys Glu Val Asp Asp Cys Pro Ile Gly Thr Asp Cys Glu Lys  
239 450 455 460  
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246 <211> LENGTH: 1422  
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254 <400> SEQUENCE: 4  
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257 gacgacaagg ttgtagaagc acttgggtgt cttgtatgt aactgtctaac cgaacatgtg 180  
258 tgtaacaaat caacgatcac tcagctacag caggagatca tcttgacaac ccacaatgaa 240  
259 ttacgaagat cattggctt cggaaagcaa agaaaacaaga gaggtctcat gaacgggtcg 300  
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262 aagcgtttct atttttatgt tgatgggcac gactctactg tacatatgcg aaacgcgtatg 480  
263 aagtattggc ggcagcaagg tgaagaaaaa ggcaatgagg atcagaaaaa tagattctat 540  
264 gccagacgaa attatttgg atgggcaaac atggcaaaag gaaaaacata tcgagttgga 600  
265 tgctcgtata ttatgtgcgg cgacgggtgaa tctgcacttt tcacttgct ttataacgaa 660  
266 aaagcccaat gcgaaaaaga aatgattac gaaaatggaa aaccctgctg tgaggataaa 720  
267 gactgttca catatccagg atcaaaatgt ttagtacctg aaggattatg tcaagcacct 780

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 270 gaatggaatg gagaaacaaa cacttccag ccaaaggcta gtcaaattgt caaaatggag 960  
 271 tatgactgca tggttggaaacg gtttgcacaa aactggcaa ataattgcgt tttgcacac 1020  
 272 tcggcacatt acgaaagacc gaatcaggtt cagaatctt acatgagttc tttctcaaac 1080  
 273 cctgatccta gaaggcttat acatacggcc gtcgagaagt ggtggcagga attggaggag 1140  
 274 ttcggtactc caattgataa cggttgcaca cccgaattgt gggattgaa agggaaagcg 1200  
 275 ataggacatt acactcagat ggcctggat cgtacttacc gtcttggttg tggaatcgca 1260  
 276 aactgtccga agatgtcgta cgtggttgt cactatgggc cagcaggcaa cagaaagaac 1320  
 277 aataaaatct atgaaatcgg ggatccttgc gaagtcgtatg atgattgccc gattggaaca 1380  
 278 gattgtgaaa agacaacttc tttatgtgtg atctcaaaat aa 1422  
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 282 <211> LENGTH: 218  
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 284 <213> ORGANISM: Artificial Sequence  
 286 <220> FEATURE:  
 287 <223> OTHER INFORMATION: Description of Artificial Sequence:Clustal W  
 288 Alignment of VAP-1, VAP-2, and Selected Other  
 289 Nematode VA Proteins.  
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 296 20 25 30  
 298 Thr Asp Lys Asp Arg Gln Ala Phe Leu Asp Phe His Asn Asn Ala Arg  
 299 35 40 45  
 301 Arg Arg Val Ala Lys Gly Val Glu Asp Ser Asn Ser Gly Lys Leu Asn  
 302 50 55 60  
 304 Pro Ala Lys Asn Met Tyr Lys Leu Ser Trp Asp Cys Ala Met Glu Gln  
 305 65 70 75 80  
 307 Gln Leu Gln Asp Ala Ile Gln Ser Cys Pro Ser Ala Phe Ala Gly Ile  
 308 85 90 95  
 310 Gln Gly Val Ala Gln Asn Val Met Ser Trp Ser Ser Ser Gly Gly Phe  
 311 100 105 110  
 313 Pro Asp Pro Ser Val Lys Ile Glu Gln Thr Leu Ser Gly Trp Trp Ser  
 314 115 120 125  
 316 Gly Ala Lys Lys Asn Gly Val Gly Pro Asp Asn Lys Tyr Asn Gly Gly  
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 319 Gly Leu Phe Ala Phe Ser Asn Met Val Tyr Ser Glu Thr Thr Lys Leu  
 320 145 150 155 160  
 322 Gly Cys Ala Tyr Lys Val Cys Gly Thr Lys Leu Ala Val Ser Cys Ile  
 323 165 170 175  
 325 Tyr Asn Gly Val Gly Tyr Ile Thr Asn Gln Pro Met Trp Glu Thr Gly  
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**VERIFICATION SUMMARY**

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